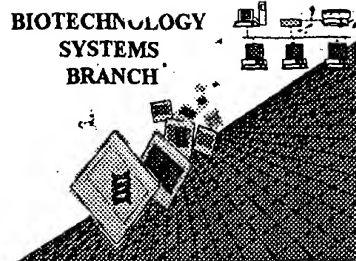


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/607,361A  
Source: OIR  
Date Processed by STIC: 7/31/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

## RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/607,361A

TIME: 13:12:01

Input Set : A:\SeqList.wpd

Output Set: N:\CRF3\07312001\I607361A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: SHIGEMORI, Yasushi  
 4 OISHI, Michio  
 6 <120> TITLE OF INVENTION: LIGATION OF DOUBLE-STRANDED DNAS  
 8 <130> FILE REFERENCE: 032735-003  
 10 <140> CURRENT APPLICATION NUMBER: US 09/607,361A  
 11 <141> CURRENT FILING DATE: 2000-06-30  
 13 <150> PRIOR APPLICATION NUMBER: JP 11-189211  
 14 <151> PRIOR FILING DATE: 1999-07-02  
 16 <160> NUMBER OF SEQ ID NOS: 14  
 18 <170> SOFTWARE: PatentIn Ver. 2.0

pp 1,3-4

(see 1.823 of sequence  
rules)

## ERRORED SEQUENCES

154 <210> SEQ ID NO: 11  
 155 <211> LENGTH: 23  
 E--> 156 <212> TYPE: ~~double stranded~~ DNA  
 157 <213> ORGANISM: Artificial Sequence  
 159 <220> FEATURE:  
 160 <223> OTHER INFORMATION: Description of double stranded sequence (DNA 1) recited in  
 Figure 1.

just show either DNA or RNA

162 <400> SEQUENCE: 11  
 163 ctagtatcgg acgacgacaa gat  
 164 ~~gatcatagcc tgctgctggt cta~~  
 166 <210> SEQ ID NO: 12  
 167 <211> LENGTH: 23  
 E--> 168 <212> TYPE: ~~double stranded~~ DNA  
 169 <213> ORGANISM: Artificial Sequence  
 171 <220> FEATURE:  
 172 <223> OTHER INFORMATION: Description of double stranded sequence (DNA 2) recited in  
 Figure 1.

delete Per 1.822 of sequence rules, show a  
single strand  
only

174 <400> SEQUENCE: 12  
 175 gacgacgaca agatgatcat gat  
 176 ~~ctagta cta~~  
 178 <210> SEQ ID NO: 13  
 179 <211> LENGTH: 32  
 E--> 180 <212> TYPE: ~~double stranded~~ DNA  
 181 <213> ORGANISM: Artificial Sequence  
 183 <220> FEATURE:  
 184 <223> OTHER INFORMATION: Description of double stranded sequence (DNA (1+2)) recited  
 in Figure 1.

23

186 <400> SEQUENCE: 13  
 187 ctagtatcgg acgacgacaa gatgatcatg at  
 188 ~~gatcatagcc tgctgctggt ctaactagtae ta~~  
 190 <210> SEQ ID NO: 14  
 191 <211> LENGTH: 10  
 E--> 192 <212> TYPE: ~~double stranded~~ DNA  
 193 <213> ORGANISM: Artificial Sequence

32

195 <220> FEATURE:

196 <223> OTHER INFORMATION: Description of double stranded sequence recited in Figure 2.

RAW SEQUENCE LISTING

DATE: 07/31/2001

PATENT APPLICATION: US/09/607,361A

TIME: 13:12:01

Input Set : A:\SeqList.wpd

Output Set: N:\CRF3\07312001\I607361A.raw

198 <400> SEQUENCE: 14

199 aaaaaaaaaa

10

200 ~~aaaaaaaa~~ *delete*

<210> 1  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthesized by referring to the random sequence 13mer that does not contain T, and the following sequence of one end of the exon 11 region of p53 gene within the human genomic DNA

<400> 1  
 gacgacgaca agacacctga agtccaaaaa gggtcagtc

<210> 2  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthesized by referring to the random sequence 14mer that does not contain T, and the following sequence of one end of the exon 11 region of p53 gene within the human genomic DNA

<400> 2  
 gaggagaagc ccggtggcag caaagtttta ttgtaaaata

more up - p53 1.823 of

sequence

rules a

maximum of

4 lines

allowed for

<223> response

same

even

40

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/607,361A

DATE: 07/31/2001

TIME: 13:12:02

Input Set : A:\SeqList.wpd

Output Set: N:\CRF3\07312001\I607361A.raw

L:30 M:259 W: Allowed number of lines exceeded, <223> Other Information:

L:45 M:259 W: Allowed number of lines exceeded, <223> Other Information:

L:156 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:168 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:180 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:192 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: